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## SEQUENCE LISTING

<110> Gabriel Vogeli  
Linda S. Wood

<120> G PROTEIN COUPLED RECEPTOR EXPRESSED IN BRAIN

<130> 28341/6202NCP

<140> US 09/634,109

<141> 2000-08-08

<150> US 09/377,563

<151> 2000-08-19

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(945)

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atg gga aga tgg gtg aac cag tcc tac aca gat ggc ttc ttc ctc ttg 48  
Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
1 5 10 15

ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96  
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val  
20 25 30

atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144  
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
35 40 45

ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc 192  
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu  
50 55 60

agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca 240  
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro  
65 70 75 80

aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg 288  
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
85 90 95

ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag 336  
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu  
100 105 110

ggg ctc ttg ctg gga ctc atg gct tat gac cac tac gtg gcc gtt agc 384  
Gly Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser  
115 120 125

cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag	432
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln	
130 135 140	
att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag	480
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln	
145 150 155 160	
atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat	528
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp	
165 170 175	
cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac	576
His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp	
180 185 190	
act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt	624
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu	
195 200 205	
ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc cta ggg	672
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly	
210 215 220	
gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg gcc	720
Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala	
225 230 235 240	
acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca gcc	768
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala	
245 250 255	
atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat gac	816
Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp	
260 265 270	
aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac ccc	864
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro	
275 280 285	
ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg aag	912
Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys	
290 295 300	
ggg ctg gac cgc tgc agg att ggc agc cag cac tga	948
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His	
305 310 315	

<210> 2

<211> 315

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
1 5 10 15

Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
20 25 30

Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe

35					40					45					
Leu	Ile	Tyr	Leu	Asp	Ala	Gly	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
50						55					60				
Ser	Gln	Leu	Ser	Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Asn	Ile	Val	Pro
65					70					75					80
Lys	Met	Ala	Ala	Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val
				85					90					95	
Gly	Cys	Gly	Ile	Gln	Ile	Gly	Phe	Phe	Val	Ser	Leu	Val	Gly	Ser	Glu
			100					105					110		
Gly	Leu	Leu	Leu	Gly	Leu	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Val	Ser
			115				120					125			
His	Pro	Leu	His	Tyr	Pro	Ile	Leu	Met	Asn	Gln	Arg	Val	Cys	Leu	Gln
	130					135					140				
Ile	Thr	Gly	Ser	Ser	Trp	Ala	Phe	Gly	Ile	Ile	Asp	Gly	Val	Ile	Gln
145					150					155					160
Met	Val	Ala	Ala	Met	Gly	Leu	Pro	Tyr	Cys	Gly	Ser	Arg	Ser	Val	Asp
				165					170					175	
His	Phe	Phe	Cys	Glu	Val	Gln	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ala	Asp
			180					185					190		
Thr	Ser	Leu	Phe	Asp	Thr	Leu	Leu	Phe	Ala	Cys	Cys	Val	Phe	Met	Leu
		195				200						205			
Leu	Leu	Pro	Phe	Ser	Ile	Ile	Met	Ala	Ser	Tyr	Ala	Cys	Ile	Leu	Gly
	210					215					220				
Ala	Val	Leu	Arg	Ile	Arg	Ser	Ala	Gln	Ala	Trp	Lys	Lys	Ala	Leu	Ala
225					230					235					240
Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Ala	Ala
				245					250					255	
Met	Phe	Met	Tyr	Leu	Arg	Pro	Arg	Arg	Tyr	Arg	Ala	Pro	Ser	His	Asp
			260					265					270		
Lys	Val	Ala	Ser	Ile	Phe	Tyr	Thr	Val	Leu	Thr	Pro	Met	Leu	Asn	Pro
		275					280					285			
Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Gly	Glu	Val	Met	Gly	Ala	Leu	Arg	Lys
	290					295					300				
Gly	Leu	Asp	Arg	Cys	Arg	Ile	Gly	Ser	Gln	His					
305					310					315					

<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER  
SEQUENCE

<400> 3  
gcctctatct tctacacagt cc

22

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PRIMER  
SEQUENCE

<400> 4  
ccaaaaccta taaaccatcc

20

<210> 5  
<211> 59  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PRIMER  
SEQUENCE

<400> 5  
gcactagtaa tacgactcac tatagggaga ccaccatggg aagatgggtg aaccagtcc 59

<210> 6  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PRIMER  
SEQUENCE

<400> 6  
gactggatcc cccgggcttt tttttttttt ttgcggccgc tcagtgtctgg ctgccaatcc 60

<210> 7  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: MAP KINASE  
SUBSTRATE PEPTIDE

<400> 7  
Ala Pro Arg Thr Pro Gly Gly Arg Arg  
1 5

<210> 8  
<211> 316  
<212> PRT  
<213> Homo sapiens

<400> 8

Met	Asp	Asn	Gln	Ser	Ser	Thr	Pro	Gly	Phe	Leu	Leu	Leu	Gly	Phe	Ser	1	5	10	15
Glu	His	Pro	Gly	Leu	Gly	Arg	Thr	Leu	Phe	Val	Asp	Val	Ile	Thr	Ser	20	25	30	
Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Leu	Ile	Ile	Leu	Leu	Ser	Ala	35	40	45	
Leu	Asp	Thr	Lys	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn	Leu	50	55	60	
Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Cys	Val	Pro	Gln	Met	Leu	65	70	75	80
Ala	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr	Ile	Ser	Phe	Leu	Asp	Cys	Ser	85	90	95	
Val	Gln	Ile	Phe	Ile	Phe	Leu	Ser	Leu	Gly	Thr	Thr	Glu	Cys	Ile	Leu	100	105	110	
Met	Lys	Val	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val	Cys	Gln	Pro	Leu	115	120	125	
His	Tyr	Ala	Thr	Ile	Ile	His	Pro	Arg	Leu	Cys	Trp	Gln	Leu	Ala	Ser	130	135	140	
Val	Ala	Trp	Val	Ile	Gly	Leu	Val	Gly	Ser	Val	Val	Gln	Thr	Pro	Ser	145	150	155	160
Thr	Leu	His	Leu	Pro	Phe	Cys	Pro	Asp	Arg	Gln	Val	Asp	Asp	Phe	Val	165	170	175	
Cys	Glu	Val	Pro	Ala	Leu	Ile	Arg	Leu	Ser	Cys	Glu	Asp	Thr	Ser	Tyr	180	185	190	
Asn	Glu	Ile	Gln	Val	Ala	Val	Ala	Ser	Val	Phe	Ile	Leu	Val	Val	Pro	195	200	205	
Leu	Ser	Leu	Ile	Leu	Val	Ser	Tyr	Gly	Ala	Ile	Thr	Trp	Ala	Val	Leu	210	215	220	
Arg	Ile	Asn	Ser	Ala	Thr	Ala	Trp	Arg	Lys	Ala	Phe	Gly	Thr	Cys	Ser	225	230	235	240
Ser	His	Leu	Thr	Val	Val	Thr	Leu	Phe	Tyr	Ser	Ser	Val	Ile	Ala	Val	245	250	255	
Tyr	Leu	Gln	Pro	Lys	Asn	Pro	Tyr	Ala	Gln	Gly	Arg	Gly	Lys	Phe	Phe	260	265	270	
Gly	Leu	Phe	Tyr	Ala	Val	Gly	Thr	Pro	Ser	Leu	Asn	Pro	Leu	Val	Tyr	275	280	285	
Thr	Leu	Arg	Asn	Lys	Glu	Ile	Lys	Arg	Ala	Leu	Arg	Arg	Leu	Leu	Gly	290	295	300	
Lys	Glu	Arg	Asp	Ser	Arg	Glu	Ser	Trp	Arg	Ala	Ala					305	310	315	

<210> 9  
 <211> 223  
 <212> PRT  
 <213> Mus musculus

<400> 9  
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro  
     1                    5                    10                    15  
 Lys Met Ala Val Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Ala  
                     20                    25                    30  
 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu  
             35                    40                    45  
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser  
     50                    55                    60  
 His Pro Leu His Tyr Pro Ile Leu Met Ser Gln Lys Val Cys Leu Gln  
     65                    70                    75                    80  
 Ile Ala Gly Ser Ser Trp Ala Phe Gly Ile Leu Asp Gly Ile Ile Gln  
                     85                    90                    95  
 Met Val Ala Ala Met Ser Leu Pro Tyr Cys Gly Ser Arg Tyr Ile Asp  
             100                    105                    110  
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ala Asp  
             115                    120                    125  
 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu  
     130                    135                    140  
 Leu Leu Pro Phe Ser Ile Ile Val Thr Ser Tyr Ala Arg Ile Leu Gly  
     145                    150                    155                    160  
 Ala Val Leu Arg Met His Ser Ala Gln Ser Arg Lys Lys Ala Leu Ala  
             165                    170                    175  
 Thr Cys Ser Ser His Leu Thr Ala Val Ser Leu Phe Tyr Gly Ala Ala  
             180                    185                    190  
 Met Phe Ile Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp  
             195                    200                    205  
 Lys Val Val Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn  
     210                    215                    220

<210> 10  
 <211> 1070  
 <212> DNA  
 <213> Homo Sapiens

<400> 10  
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 agacatgtca ctcaatctta taatttctct tatgttctca ggtgacagtg aacaactaag 120  
 ccatgggaag atgggtgaac cagtccctaca cagatggctt cttcctcttg ggcatctttt 180  
 cccacagcca gactgacctt gtcctcttct ctgcagttat ggtgggtcttc acagtggccc 240  
 tctgtgggaa tgtcctcctc atcttccctca tctacctgga cgctggactt cacaccccca 300  
 tgtacttctt cctcagccag ctctccctca tggacctcat gttgggtctgt aacattgtgc 360  
 caaagatggc agccaacttc ctgtctggca ggaagtccat ctcctttgtg ggctgtggca 420  
 tacaaattgg cttttttgtc tctcttgtgg gatctgaggg gctcttgctg ggactcatgg 480

cttatgacca ctacgtggcc gttagccacc cacttcacta tcccatcctc atgaatcaga 540  
gggtctgtct ccagattact gggagctcct gggcctttgg gataatagat ggagtgattc 600  
agatgggtggc agccatgggc ttaccttact gtggctcaag gagcgtggat cactttttct 660  
gtgaggtaca agctttattg aagctggcct gtgcagacac ttcccttttt gacacctcc 720  
tctttgcttg ctgtgtcttc atgcttctcc ttcccttctc catcatcatg gcctcctatg 780  
cttgcatcct aggggctgtg ctccgaatac gctctgctca ggcttgaaa aaagccctgg 840  
ccacctgctc ctcccaccta acagctgtca ccctcttcta tggggcagcc atgttcatgt 900  
acctgaggcc taggcgctac cgggccccta gccatgacaa ggtggcctct atcttctaca 960  
cagtccttac tcccatgctg aaccccccta ttacagctt gaggaatggg gaggtgatgg 1020  
gggcactgag gaaggggctg gaccgctgca ggattggcag ccagcactga 1070

<210> 11  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide Primer

<400> 11  
tgaggatggg atagtgaagt ggggtggctaa cggccacgta gtg 43

<210> 12  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide Primer

<400> 12  
tgacatgtct ctattgtgct ccaaattctt cagttcaaca gcgtatgctc 50

<210> 13  
<211> 305  
<212> PRT  
<213> Homo sapiens

<400> 13

Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu Gly Ile Phe Ser His  
1 5 10 15

Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val Met Val Val Phe Thr  
20 25 30

Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe Leu Ile Tyr Leu Asp  
35 40 45

Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu  
50 55 60

Met Asp Leu Met Leu Val Cys Asn Ile Val Pro Lys Met Ala Ala Asn  
65 70 75 80

Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val Gly Cys Gly Ile Gln  
85 90 95

Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu Gly Leu Leu Leu Gly  
100 105 110

Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser His Pro Leu His Tyr  
115 120 125

Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln Ile Thr Gly Ser Ser  
130 135 140

Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln Met Val Ala Ala Met  
145 150 155 160

Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp His Phe Phe Cys Glu  
165 170 175

Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp Thr Ser Leu Phe Asp  
180 185 190

Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu Leu Leu Pro Phe Ser  
195 200 205

Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly Ala Val Leu Arg Ile  
210 215 220

Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala Thr Cys Ser Ser His  
225 230 235 240

Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala Met Phe Met Tyr Leu  
245 250 255

Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp Lys Val Ala Ser Ile  
260 265 270

Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
275 280 285

Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys Gly Leu Asp Arg Cys  
290 295 300

Arg  
305



<210> 14  
 <211> 223  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro  
 1 5 10 15

Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
 20 25 30

Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu  
 35 40 45

Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser  
 50 55 60

His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln  
 65 70 75 80

Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln  
 85 90 95

Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp  
 100 105 110

His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp  
 115 120 125

Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu  
 130 135 140

Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly  
 145 150 155 160

Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala  
 165 170 175

Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala  
 180 185 190

Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp  
 195 200 205

Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn  
 210 215 220

B1  
 cont.